



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 10/500173

TO: Patrick S Riggins
Location: REM-2D60&2C70
Art Unit: 1633
Monday, April 10, 2006
Case Serial Number: 10/500173

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523
toby.port@uspto.gov

Search Notes

Examiner Riggins,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:10:27 ; Search time 344.814 Seconds
(without alignment(s))
6758.955 Million cell updates/sec

Title: US-10-500-173-1

Perfect Score: 41

Sequence: 1 gaaacaatgacacatcgc.....cccaataccaaaggccgtac 41

Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_dx:*

9: gb_ro:*

10: gb_sts:*

11: gb_by:*

12: gb_un:*

13: gb_vl:*

14: gb_itg:*

15: gb_pl:*

No. Score Match Length DB ID Description

1 41 100.0 41 6 BD181246 Cell spec

2 41 100.0 41 6 BD182147 Cell spec

3 41 100.0 260 6 BD181247 Cell spec

4 41 100.0 260 6 BD182148 Cell spec

5 41 100.0 334 8 BD182148 Cell spec

6 41 100.0 333 6 BD182149 Cell spec

7 41 100.0 1221 8 DB5611 Human smooth

8 41 100.0 142645 8 AC008481

9 41 100.0 142645 8 AC008481

10 41 100.0 178388 14 AC151856 Papiro ham

11 41 100.0 224294 14 AC151861 Callicebus

c 12 39.4 96.1 163264 14 AC151891 Aotus nan

13 39.4 96.1 18174 14 AC151893 Callithrix

14 39.4 96.1 186803 14 AC151868

c 15 39.4 96.1 19952 14 AC153457

16 39.4 96.1 250810 14 AC151886 Saimiri b

17 37.8 92.2 236017 14 AC150437 Lemur cat

18 36.2 88.3 485 9 AF123268

19 36.2 88.3 1216 9 NM001001

20 36.2 88.3 3001 9 NM037071

21 36.2 88.3 10373 9 MUS1CA

22 36.2 88.3 174533 14 AC073718

c 23 36.2 88.3 170592 14 AC144892

24 36.2 88.3 194267 14 AC163623

25 36.2 88.3 195394 14 AC051223

26 36.2 88.3 201374 14 AC073786

27 36.2 88.3 236385 14 AC084744

c 28 36.2 88.3 243292 14 AC132732

29 34.6 88.4 20723 14 AC145342

30 25.6 62.4 230705 14 AC130936

c 31 24.2 59.0 171332 8 AC110760

32 24.2 59.0 220801 9 AC124604

c 33 24 58.5 263227 14 AC095809

34 23.6 57.6 110000 1 AC000031_19

c 35 23.6 57.6 133128 5 BX76083

36 23.6 57.6 149330 14 CR628386

c 37 23.6 57.6 153943 14 AC027417

38 23.6 57.6 157544 8 AC098590

c 39 23.6 57.6 170443 14 AC048384

40 23.2 56.6 58359 14 AC148218

c 41 23.2 56.6 209456 14 AC114696

c 42 23.2 56.6 214942 9 AC125214

c 43 23.2 56.6 227767 14 AC118766

c 44 23.2 56.6 228505 14 AC111714

c 45 23 56.1 9990 1 AC002243

ALIGNMENTS

RESULT 1
BD181246

LOCUS Cell specific express replication vector.

DEFINITION BD181246

ACCESSION BD181246

VERSION GI:30792164

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Butaleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 41)

AUTHORS Takahashi, K., Yamamura, H. and Miyatake, S.

TITLE Cell specific express replication vector.

JOURNAL Patent: JP 2002335965-A 1 26-NOV-2002; JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)

PN JP 2002335965-A/1

PD 26-NOV-2002

PP 14-MAY-2001 JP 2001143999

PI KATSUHITO TAKAHASHI, HISAKO YAMAMURA, SHINICHI MIYATAKE PC

C12N15/09, A61K35/76, A61K48/00, AC1P35/00, C12N15/00, PC

C12N15/00

CC Cell specific express replication vector

PH Key Location/Qualifiers

FT Source 1..41

FT Location/Qualifiers

FT Source 1..41

FT /organism="Homo sapiens" (human)

FEATURES Source 1..41

FT /organism="Homo sapiens"

FT /mol_type="genomic DNA"

FT /db_xref="taxon:9606"

ORIGIN

Query Match Length DB ID Description

1 41 100.0 41 6 BD181246 Cell spec

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10 41 100.0 224294 14 AC151861 Callicebus

<p

GenCore version 5.1.7
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DNM nucleic - nucleic search, using sw model
 run on: April 9, 2006, 02:04:37 ; Search time 59.4306 seconds
 (without alignments) 4597.840 Million cell updates/s

title: US-10-500-173-1
 perfect score: 41
 sequence: 1 gaaacatgacaaatcagc.....cccaaatccaaagggtgac 41

scoring table: IDENTITY NUC
 GapOp 10.0 , GapExt 1.0

searched: 4996397 seqs, 3332346308 residues

total number of hits satisfying chosen parameters: 9993994

minimum DB seq length: 0
 maximum DB seq length: 200000000
 post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : N_Geneseq_21;*
 |_Geneseq_10000;*

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1: geneseqn1990s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn201bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *

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Result No.	Score	Query			Length	DB	ID	Description
		Match	Length	DB				
1	41	100.0	41	10	ADC21270	Human	Abc21270	Human
2	41	100.0	41	10	ADD63309	Human	Add63309	Human
3	41	100.0	41	10	ADD28393	Antia	Add28393	Antia
4	41	100.0	41	10	ABZ70044	Oligo	Abz70044	Oligo
5	41	100.0	260	10	ADC21271	Human	Adc21271	Human
6	41	100.0	260	10	ADD68310	Human	Add68310	Human
7	41	100.0	260	10	ADD28394	Antia	Add28394	Antia
8	41	100.0	260	10	ABZ70045	Oligo	Abz70045	Oligo
9	41	100.0	333	10	ADC21272	Human	Adc21272	Human
10	41	100.0	333	10	ADD68311	DNA cc	Add68311	DNA cc
11	41	100.0	333	10	ADD29395	Human	Add29395	Human
12	41	100.0	333	10	ABZ70046	Human	Abz70046	Human
c	23	56.1	11.0000	2	AAX1990	Continuation (11)	Aax1990	Continuation (11)
c	22.2	54.1	780	8	ACA40205	Prokary	Aca40205	Prokary
c	15	53.7	652	8	AAX19896	Mouse	Aax19896	Mouse
c	16	53.7	2293	2	AAX19900	Plasmid	Aax19900	Plasmid
c	17	53.2	168276	11	ACM43942	Human	Acn43942	Human

סימן 15: איזה?

RESULT 1	
ADC21270	ADC21270 standard; DNA; 41 BP.
XX	
AC	ADC21270;
XX	18-DRC-2003 (first entry)
XX	Human cell-specific expression vector-related DNA sequence #1.
KW	human; cell-specific expression vector; cell-specific replication vector;
KW	gene therapy; malignant tumour; liver fibrosis; postoperative scarring;
KW	organ transplantation; arteriosclerosis; diabetic omentopathy; ds.
KW	

OS Homo sapiens.
 XX
 PN WO2013057888-A1.
 XX
 PD 17-JUL-2003.
 XX
 PP 26-DEC-2002; 2002WO-JP013683.
 XX
 PR 28-DEC-2001; 2001JP-00402102.
 PR 30-AUG-2002; 2002JP-00255395.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Takahashi K, Yamamura H;
 XX
 DR WPI; 2003-577527/54.
 XX
 PT Cell-specific expression/replication vector containing transcription
 PT initiation regulating domain of human calponin gene, applicable in gene
 PT therapy of malignant tumor lung and liver fibrosis or diabetic
 PT omentopathy.
 XX
 PS Claim 2; SEQ ID NO 1; 66pp; Japanese.
 XX
 CC The invention comprises a cell-specific expression/replication vector
 CC which does not act on normal cells. The vector of the invention is useful
 CC in gene therapy for the treatment of: malignant tumour, liver fibrosis,
 CC postoperative stenosis (e.g. stenosis after organ transplantation),

Result No.	Score	Query	Match	Length	DB ID	Description	Source
c 1	24.2	95.9	59.0	578	9 A2954724	A2954724 2N0220101	CB577767 AMGNNUC:U
c 2	24.2	95.9	59.0	687	2 BB636761	BB636761 BB636361	CW332222 104_829_1
c 3	24.2	95.9	59.0	817	8 CX705942	CX705942 SmtdDNs0	CW332223 104_829_1
c 4	24	95.8	58.5	578	2 BG887927	W887927 EST513778	DR917045 EST110858
c 5	23.2	95.6	56.6	455	8 W81232	W81232 zdb85907_81	BZ988727 PUGHp347B
c 6	23.2	95.6	56.6	457	8 DN589073	DN589073 4998.1 L	CC350006 OGIAx91TH
c 7	23.2	95.6	56.6	457	8 DR037737	DR037737 4998.2 L	CG106814 PUFVB867B
c 8	23.2	95.6	56.6	457	8 DR037738	DR037738 4998.3 L	CL292836 2MmBB064
c 9	23.2	95.6	56.6	465	1 A1773494	A1773494 EST254594	CC364981 PUEBC657D
c 10	23.2	95.6	56.6	580	1 A1170292	A1170292 EST216218	CG598900 EST5031788
c 11	23.2	95.6	56.6	624	2 BG598900	BG598900 EST5031788	BQ046841 EST599959
c 12	23.2	95.6	56.6	736	3 BQ046841	BQ046841 EST599959	CD002122 EST0119 N
c 13	23	95.6	56.1	403	6 CD003495	CD003495 RZ1483B0	CD603495 RZ1483B0
c 14	23	95.6	56.1	429	6 BM403754	BM403754 ram160 2	BM403754 ram160 2
c 15	23	95.6	56.1	444	3 BM881674	BM881674 BW881674	BW881674 BW881674
c 16	23	95.6	56.1	486	5 BG799583	BG799583 fo8hb03.Y	BG799583 fo8hb03.Y
c 17	23	95.6	56.1	489	2 BG799583	AQB91537 HS_3063_A	AQB91537 HS_3063_A
c 18	23	95.6	56.1	571	9 AQB91537	CB43759 CA3759	CB43759 CA3759
c 19	23	95.6	56.1	644	6 CFB232494	CFB232494 PtaxJX0001	CFB232494 PtaxJX0001
c 20	23	95.6	56.1	732	6 CFB232494	BZ773339 mcv78D08.	BZ773339 mcv78D08.
c 21	23	95.6	56.1	760	9 BZ773339	AG341458 Mus muscu	AG341458 Mus muscu
c 22	23	95.6	56.1	1246	10 AG341458		

Post-processing: Minimum Match 0\$
 Maximum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100\$
 Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	41	100.0	15585	3	US-09-949-016-11927		Sequence 11927, A
2	41	100.0	15585	3	US-09-949-016-15627		Sequence 15627, A
C	3	56.1	12302305	3	US-09-198-452A-1		Sequence 1, Appl
C	4	23	56.1	1230230	3	US-09-438-185A-1	Sequence 1, Appl
C	5	21.8	53.2	601	3	US-09-949-016-13708	Sequence 130708, A
C	6	21.8	53.2	42250	3	US-09-949-016-15426	Sequence 1526, A
C	7	21.6	52.7	601	3	US-09-949-016-196661	Sequence 196661, A
C	8	21.6	52.7	28585	3	US-09-949-016-17311	Sequence 17311, A
C	9	21	51.2	209210	3	US-09-949-016-15094	Sequence 15094, A
C	10	20.8	50.7	456	3	US-09-328-352-B2	Sequence 82, Appl
C	11	20.8	50.7	601	3	US-09-949-016-10354	Sequence 10354,
C	12	20.8	50.7	601	3	US-09-949-016-103355	Sequence 103355,
C	13	20.8	50.7	601	3	US-09-949-016-127545	Sequence 127545,
C	14	20.8	50.7	723	3	US-09-328-352-298	Sequence 298, Appl
C	15	20.8	50.7	2904	3	US-09-054-272-29	Sequence 29, Appl
C	16	20.8	50.7	4450	3	US-09-949-016-2850	Sequence 2850, Appl
C	17	20.8	50.7	4510	3	US-09-949-016-14604	Sequence 16, Appl
C	18	20.8	50.7	34531	3	US-09-949-016-14604	Sequence 1604, A
C	19	20.8	50.7	36223	3	US-09-949-016-14417	Sequence 14417, A
C	20	20.8	50.7	73757	3	US-09-949-016-15369	Sequence 15369, A
C	21	20.6	50.2	50109	3	US-09-194-016-14112	Sequence 1112, A
C	22	20.6	50.2	98708	3	US-09-949-016-16392	Sequence 16392, A
C	23	20.4	49.8	601	3	US-09-949-016-64221	Sequence 64221, A
C	24	20.4	49.8	981	3	US-09-270-767-956	Sequence 956, App

ALIGNMENTS

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 / Sequence 11927, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / PRIORITY APPLICATION NUMBER: 60/241,755
 / CURRENT FILING DATE: 2000-04-14
 / PRIORITY FILING DATE: 2000-10-20
 / PRIORITY APPLICATION NUMBER: 60/237,768
 / PRIORITY FILING DATE: 2000-10-03
 / PRIORITY APPLICATION NUMBER: 60/231,498
 / PRIORITY FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 20012
 / SOFTWARE: FastBQ for Windows Version 4.0
 / SEQ ID NO: 11927
 / LENGTH: 15585
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (1) ..(15585)
 / OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-11927

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 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
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 Db 1819 GAACAATGACAGATAGCTCCAAATACCAACGGCTGAC 1859

RESULT 2
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 / Sequence 15627, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:22:52 : Search time 96.2918 Seconds

(without alignments)
 3521.011 Million cell updates/sec

Title: US-10-500-173-1

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 Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs. 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA_Main.*
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	41	100.0	41	8 US-10-500-173-1	Sequence  Appli
3	41	100.0	260	8 US-10-477-797-2	Sequence  Appli
4	41	100.0	260	8 US-10-500-173-2	Sequence  Appli
5	41	100.0	333	8 US-10-477-797-3	Sequence  Appli
6	41	100.0	333	8 US-10-500-173-3	Sequence  Appli
C 7	24.2	59.0	297	7 US-10-424-599-2981	Sequence  Appli
C 8	23.6	57.6	616	4 US-10-925-065A-886727	Sequence  Appli
C 9	23	56.1	1230025	6 Sequence  Appli	
C 10	22.6	55.1	554	5 US-10-289-767-1	Sequence  Appli
C 11	22.6	55.1	554	5 US-10-027-632-25758	Sequence  Appli
C 12	22.6	55.1	554	5 US-10-027-632-265760	Sequence  Appli
C 13	22.6	55.1	554	6 US-10-027-632-25758	Sequence  Appli
C 14	22.6	55.1	554	6 US-10-027-632-265759	Sequence  Appli
C 15	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 16	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 17	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 18	22.4	54.6	526	5 US-10-027-632-273806	Sequence  Appli
C 19	22.4	54.6	526	6 US-10-027-632-273806	Sequence  Appli
C 20	22.4	54.6	530	4 US-09-925-065A-592112	Sequence Appli
C 21	22.4	54.6	530	4 US-09-925-065A-592113	Sequence Appli
C 22	22.4	54.6	530	4 US-09-925-065A-592114	Sequence Appli
C 23	22.4	54.6	574	4 US-09-925-065A-411954	Sequence Appli

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	41	100.0	333	8 US-10-477-797-3	Sequence  Appli
C 6	24.2	59.0	297	7 US-10-424-599-2981	Sequence  Appli
C 7	23.6	57.6	616	4 US-10-925-065A-886727	Sequence  Appli
C 8	23	56.1	1230025	6 Sequence  Appli	
C 9	22.6	55.1	554	5 US-10-289-767-1	Sequence  Appli
C 10	22.6	55.1	554	5 US-10-027-632-25758	Sequence  Appli
C 11	22.6	55.1	554	5 US-10-027-632-265759	Sequence  Appli
C 12	22.6	55.1	554	6 US-10-027-632-25758	Sequence  Appli
C 13	22.6	55.1	554	6 US-10-027-632-265759	Sequence  Appli
C 14	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 15	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 16	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 17	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
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C 21	22.4	54.6	530	4 US-09-925-065A-592113	Sequence  Appli
C 22	22.4	54.6	530	4 US-09-925-065A-592114	Sequence  Appli
C 23	22.4	54.6	574	4 US-09-925-065A-411954	Sequence  Appli

Result No.	Score	Query Match	Length	DB ID	Description
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5	41	100.0	333	8 US-10-477-797-3	Sequence  Appli
C 6	24.2	59.0	297	7 US-10-424-599-2981	Sequence  Appli
C 7	23.6	57.6	616	4 US-10-925-065A-886727	Sequence  Appli
C 8	23	56.1	1230025	6 Sequence  Appli	
C 9	22.6	55.1	554	5 US-10-289-767-1	Sequence  Appli
C 10	22.6	55.1	554	5 US-10-027-632-25758	Sequence  Appli
C 11	22.6	55.1	554	5 US-10-027-632-265759	Sequence  Appli
C 12	22.6	55.1	554	6 US-10-027-632-25758	Sequence  Appli
C 13	22.6	55.1	554	6 US-10-027-632-265759	Sequence  Appli
C 14	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 15	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 16	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 17	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 18	22.4	54.6	526	5 US-10-027-632-273806	Sequence  Appli
C 19	22.4	54.6	526	6 US-10-027-632-273806	Sequence  Appli
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C 21	22.4	54.6	530	4 US-09-925-065A-592113	Sequence  Appli
C 22	22.4	54.6	530	4 US-09-925-065A-592114	Sequence  Appli
C 23	22.4	54.6	574	4 US-09-925-065A-411954	Sequence  Appli

Result No.	Score	Query Match	Length	DB ID	Description
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C 13	22.6	55.1	554	6 US-10-027-632-265759	Sequence  Appli
C 14	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 15	22.6	55.1	554	6 US-10-027-632-265760	Sequence  Appli
C 16	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 17	22.4	54.6	472	4 US-09-925-065A-591663	Sequence  Appli
C 18	22.4	54.6	526	5 US-10-027-632-273806	Sequence  Appli
C 19	22.4	54.6	526	6 US-10-027-632-273806	Sequence  Appli
C 20	22.4	54.6	530	4 US-09-925-065A-592112	Sequence  Appli
C 21	22.4	54.6	530	4 US-09-925-065A-592113	Sequence  Appli
C 22	22.4	54.6	530	4 US-09-925-065A-592114	Sequence  Appli
C 23	22.4	54.6	574	4 US-09-925-065A-411954	Sequence  Appli

Result No.	Score</

Copyright (c) 1993 - 2006 Biocceleration Ltd.	Gencore version 5.1.7	AC145542	Oryctolag			
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Listing first 45 summaries		c	BD181246			
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
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c	10	184.6	71.0	186603	H.sapiens	
c	11	181.4	69.4	181714	AC151868	
c	12	179.8	69.2	250510	Actus nan	
c	13	178.2	68.5	163264	AC151861	
c	14	168.4	64.8	236017	Colobus	
c	15	164	63.1	1600	AC151866	
c	16	164	63.1	1605	Papio ham	
c	17	157	57.7	1633	AC151868	
c	18	142	56.4	169562	Callithri	
c	19	134.2	51.6	207823	Actus nan	
c	20	101	38.8	245942	AC151866	
c	21	100	38.5	15222	Saimiri b	
c	22	93.6	36.0	10373	AC151861	
c	23	93.6	36.0	174533	Callithri	
c	24	93.6	36.0	194267	Actus nan	
c	25	93.6	36.0	195294	AC151866	
c	26	93.6	36.0	201371	Callithri	
c	27	93.6	36.0	236685	Actus nan	
c	28	92	35.4	1517	AC073718	
c	29	92	35.4	1517	Mus muscu	
c	30	92	35.4	1517	AC163623	
c	31	87.4	33.6	485	AC051623	
c	32	84.2	32.4	3001	MMU17071	
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					Takahashi, K., Yamamura, H. and Miyatake, S.	
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					AUTHORS	
					Takahashi, K., Yamamura, H. and Miyatake, S.	
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					CC	
					KEY	
					FT	
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					Best Local Similarity 100.0%	
					Mismatches 0;	
					Indels 0;	
					Gaps 0;	
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:04:37 ; Search time 376.877 Seconds

Title: US-10-500-173-2
Perfect score: 260
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Scoring table: IDENTITY_NUC
Gapp 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB. ID	Description
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3	260	100.0	260	10	ADD23394	Add29394 Antiarter
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5	260	100.0	333	10	ADC21272	Add21272 Human cel
6	260	100.0	333	10	ADD68311	Add68311 DNA Compr
7	260	100.0	333	10	ADD29395	Add29395 Human cel
8	260	100.0	333	10	ABZ70046	ABZ70046 Human cel
9	213	81.9	1206	13	ACN1242	ACN1242 Human dia
10	213	81.9	1257	13	ACN1241	ACN1241 Human dia
11	213	81.9	1395	13	ACN1239	ACN1239 Human dia
12	213	81.9	1395	13	ACN1240	ACN1240 Human dia
13	164	63.1	1605	12	ADN04009	ADN04009 Antisori
14	135	51.9	1586	10	ADJ56427	ADJ56427 Human cDN
15	100	38.5	1522	2	AAQ86719	AAQ86719 Carponin
16	100	38.5	1522	2	AT18663	AT18663 Carponin
17	92	35.4	1517	6	ABL62318	ABL62318 Colon ade
18	92	35.4	1517	6	ABL63488	ABL69488 Prostate
19	35.4	1517	6	ABT10830	ABT10830 Human bre	

Alignments

RESULT 1
ID ADC21271
ID ADC21271 standard; DNA; 260 BP.
XX
AC ADC21271;
XX
DT 18-DEC-2003 (first entry)
XX

Human cell-specific expression vector-related DNA sequence #2.
DB Human; cell-specific expression vector; cell-specific replication vector;
XX human; cell-specific expression vector; malignant tumour; liver fibrosis; postoperative stenosis;
KW gene therapy; organ transplantation; arteriosclerosis; diabetic omentopathy; ds.
XX
DE Human cell-specific expression vector.
XX
KW human; cell-specific expression vector; cell-specific replication vector;
KW gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
KW organ transplantation; arteriosclerosis; diabetic omentopathy; ds.
XX
OS Homo sapiens.
XX
PN WO2003057888-A1.
XX
PD 17-JUL-2003.
XX
PP 26-DEC-2002; 2002WO-JP013683.
XX
PR 28-DEC-2001; 2001JP-00402102.
PR 30-AUG-2002; 2002JP-00255395.
PA (NISCS-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Takahashi K, Yamamura H;
XX
DR WPT; 2003-577527/54.
XX
PT Cell-specific expression/relication vector containing transcription
initiating domain of human calponin gene, applicable in gene
therapy of malignant tumor lung and liver fibrosis or diabetic
omentopathy.
XX
PS Claim 3; SEQ ID NO 2; 66pp; Japanese.
XX
CC The invention comprises a cell-specific expression/relication vector
which does not act on normal cells. The vector of the invention is useful
in gene therapy for the treatment of: malignant tumour, liver fibrosis,
CC postoperative stenosis (e.g. stenosis after organ transplantation),

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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 13:46:44 ; Search time 127.95 Seconds

(without alignments)
3612.096 Million cell updates/sec

Title: US-10-500-173-2
Perfect score: 260

Sequence: 1 gaaacatgacacaatcagc.....gcagagccacggccagc 260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6_ptodata/1/ina/1_COMB.seq:
2: /cgn2_6_ptodata/1/ina/5_COMB.seq:
3: /cgn2_6_ptodata/1/ina/5A_COMB.seq:
4: /cgn2_6_ptodata/1/ina/H_COMB.seq:
5: /cgn2_6_ptodata/1/ina/BCTUS_COMB.seq:
6: /cgn2_6_ptodata/1/ina/BCTUS_COMB.seq:
7: /cgn2_6_ptodata/1/ina/RE_COMB.seq:
8: /cgn2_6_ptodata/1/ina/RE_COMB.seq:
9: /cgn2_6_ptodata/1/ina/backfile1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	260	100.0	15585	3	US-09-949-016-11927	Sequence 11927, A	
2	260	100.0	15585	3	US-09-949-016-15627	Sequence 15627, A	
3	78	30.0	1504	3	US-09-949-016-3885	Sequence 3885, AP	
4	36.8	14.2	8186	3	US-09-949-016-185	Sequence 185, AP	
C	5	36	13.3	120	US-09-029-517-19	Sequence 19, App1	
6	34.6	13.3	601	3	US-09-949-016-14341	Sequence 4341, AP	
7	34.6	13.3	3510	3	US-09-949-016-169734	Sequence 169734, AP	
8	34.6	13.3	5962	9	US-09-265-585C-95	Sequence 95, App1	
C	9	34.6	13.3	5386225-5	Patent No. 5386025	Patent No. 5386025	
C	10	34.6	13.3	5975	2	US-08-404-354B-1	Sequence 1, App1
C	11	34.6	13.3	5975	2	US-08-314-083B-1	Sequence 1, App1
C	12	34.6	13.3	5975	2	US-08-435-675B-1	Sequence 1, App1
C	13	34.6	13.3	5975	2	US-08-336-257A-3	Sequence 3, App1
C	14	34.6	13.3	5975	3	US-08-884-599-1	Sequence 1, App1
C	15	34.4	13.2	23187	3	US-09-499-1522-1	Sequence 1, App1
C	16	33.4	12.8	601	3	US-09-949-016-169736	Sequence 169736,
C	17	33.4	12.8	2400	3	US-08-930-001-1	Sequence 1, App1
C	18	33.4	12.8	2400	3	US-09-091-885-1	Sequence 1, App1
C	19	33.4	12.8	18079	3	US-09-949-016-13344	Sequence 13344, A
C	20	33.4	12.8	99748	3	US-09-949-016-11990	Sequence 11990, A
C	21	33.4	12.8	99749	3	US-09-165-169518	Sequence 16518, A
C	22	33	12.7	342	3	US-09-893-737-93	Sequence 93, App1
C	23	33	12.7	601	3	US-09-949-016-55187	Sequence 55187, A
C	24	33	12.7	601	3	US-09-949-016-55188	Sequence 55188, A

ALIGNMENTS

C	25	33	12.7	601	3	US-09-949-016-169735	Sequence 169735,
C	26	33	12.7	675	3	US-09-252-991A-5532	Sequence 5532, AP
C	27	33	12.7	1485	3	US-09-252-991A-5638	Sequence 5638, AP
C	28	33	12.7	3321	3	US-09-252-991A-5568	Sequence 5568, AP
C	29	32.6	12.5	690	3	US-09-103-840A-2	Sequence 2, App1,
C	30	32.4	12.5	4403765	3	US-09-103-840A-2	Sequence 2, App1,
C	31	32.4	12.5	441159	3	US-09-232-463-14	Sequence 14, App1
C	32	32.2	12.4	7218	2	US-09-232-463-14	Sequence 14, App1
C	33	32	12.3	10465	3	US-09-949-016-13136	Sequence 13136, A
C	34	31.8	12.2	601	3	US-09-949-016-91943	Sequence 91943, A
C	35	31.8	12.2	601	3	US-09-949-016-194884	Sequence 194884,
C	36	31.8	12.2	601	3	US-09-949-002-3572	Sequence 3572, AP
C	37	31.8	12.2	601	3	US-09-949-002-6250	Sequence 6250, AP
C	38	31.8	12.2	601	3	US-09-949-002-10314	Sequence 10314, A
C	39	31.8	12.2	601	3	US-09-949-002-10314	Sequence 10314, A
C	40	31.8	12.2	1510	2	US-08-300-193-12	Sequence 12, App1
C	41	31.8	12.2	1510	3	US-08-988-197-12	Sequence 12, App1
C	42	31.8	12.2	1510	3	US-10-385-72-12	Sequence 12, App1
C	43	31.8	12.2	14395	3	US-09-949-016-12247	Sequence 12247, A
C	44	31.8	12.2	14395	3	US-09-949-016-16357	Sequence 16357, A
C	45	31.8	12.2	14688	3	US-09-949-016-12220	Sequence 12220, A

ALIGNMENTS

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RESULT 1
US-10-477-797-2
; Sequence 2, Application US/10477797
; Publication No. US20040197308A1
; GENERAL INFORMATION:
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression
; FILE REFERENCE: K01002PCT
; CURRENT APPLICATION NUMBER: US/10/477,797
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: JP P2001-143995
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-797-2

Query Match          100.0%; Score 260; DB 8; Length 260;
Best Local Similarity 100.0%; Pred. No. 3 8e-73;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy   1 GAAACAATGAAATCAAGCTCCAAATACCAAGGGCTGACATCAACAGGGAGGGAGG
Db   1 GAAACAATGAAATCAAGCTCCAAATACCAAGGGCTGACATCAACAGGGAGGGAGG
Qy   61 GCACTGAGGTTGCGGGAGGTTGCGGGAGGTTGCGGGAGGTTGCGGGAGGTTGCGGGAGG
Db   61 GCACTGAGGTTGCGGGAGGTTGCGGGAGGTTGCGGGAGGTTGCGGGAGGTTGCGGGAGG
Qy   121 CGGCCTGGAAAGAACCCGGTGCCTCGGAACCTTCAAAAATGTGAGGACCGAAAGAG
Db   121 CGGCCTGGAAAGAACCCGGTGCCTCGGAACCTTCAAAAATGTGAGGACCGAAAGAG
Qy   181 TGTGAGAGGGAACTTCAGCCGCTGCTGTTCTACCGTGTGCGGCCACTGCCCC
Db   181 TGTGAGAGGGAACTTCAGCCGCTGCTGTTCTACCGTGTGCGGCCACTGCCCC
Qy   241 GCGAGGCCACCGGCAAGC 260
Db   241 GCGAGGCCACCGGCAAGC 260

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ered. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using bw model

Run on: April 9, 2006, 02:36:12 ; Search time 479.811 Seconds
(without alignments)
2167.823 Million cell updates/sec

Title: US-10-500-173-2
Perfect score: 260
Sequence: 1 gaaacatgacacaatccatgc.....ggcagagcccccggccggcagc 260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9267305 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New:
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2: /SIDS5/ptodata/1/pubna/US06 NEW_PUB.seq:
3: /SIDS5/ptodata/1/pubna/US07 NEW_PUB.seq:
4: /SIDS5/ptodata/1/pubna/US05 NEW_PUB.seq:
5: /SIDS5/ptodata/1/pubna/US09 NEW_PUB.seq:
6: /SIDS5/ptodata/1/pubna/US10 NEW_PUB.seq:
7: /SIDS5/ptodata/1/pubna/US10 NEW_PUB.seq:
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10: /SIDS5/ptodata/1/pubna/US10 NEW_PUB.seq3:
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13: /SIDS5/ptodata/1/pubna/US11 NEW_PUB.seq3:
14: /SIDS5/ptodata/1/pubna/US11 NEW_PUB.seq4:
15: /SIDS5/ptodata/1/pubna/US60 NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	63.1	1605	14	US-11-000-688-1504 Sequence 1504, Ap
2	78	30.0	1504	11	US-11-1245-147-194 Sequence 194, App
c 3	36.8	14.2	1084	9	US-10-517-616-82 Sequence 82, App
c 4	36.8	14.2	1582	11	US-11-050-457-664 Sequence 464, App
c 5	36.8	14.2	1582	11	US-11-043-906-59 Sequence 59, App
c 6	34.8	13.4	13299	14	US-11-124-367A-5011 Sequence 5011, App
c 7	34.4	13.2	23187	11	US-11-236-198-1 Sequence 1, App1
c 8	33.6	12.9	2213	14	US-11-330-773-93 Sequence 94, App1
c 9	33.6	12.9	26563	9	US-10-330-773-93 Sequence 93, App1
c 10	33.4	12.8	133376	14	US-11-121-086-5 Sequence 5, App1
c 11	33.4	12.8	172543	14	US-11-121-086-6 Sequence 6, App1
c 12	33.2	12.8	398	11	US-11-116-881A-1686 Sequence 1616, Ap
c 13	33.2	12.8	22855	14	US-11-124-368A-2908 Sequence 2908, Ap
c 14	33	12.7	1521	14	US-11-136-527-1998 Sequence 1998, Ap
c 15	33	12.7	3752	8	US-10-750-185-28772 Sequence 28772, A
c 16	33	12.7	3752	8	US-10-750-623-34347 Sequence 34347, A
c 17	32.8	12.6	614	14	US-11-136-527-1651 Sequence 1651, Ap
c 18	32.8	12.6	978	10	US-10-301-480-1162253 Sequence 1162253, A

ALIGNMENTS

RESULT 1
US-11-000-688-1504
; Sequence 1504, Application US/11000688
; General Information:
; Publication No. US2005287544A1
; Applicant: BERTUCCI, Francois
; Applicant: HOULGARTTE, Remi
; Title of Invention: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; File Reference: 1423-R-03
; Current Application Number: US/11/000, 688
; Current Filing Date: 2004-12-01
; Prior Application Number: US 60/525, 987
; Prior Filing Date: 2003-12-01
; Number of SEQ ID NOS: 1596
; SEQ ID NO: 1504
; LENGTH: 1605
; Software: Patentin version 3.2
; Type: DNA
; Organism: Artificial Sequence
; Feature:
; Other Information: Description of Artificial sequences: primer

Query Match 63.1%; Score 164; DB 14; Length 1605;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 164; Conserv 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 63.1%; Score 164; DB 14; Length 1605;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 164; Conserv 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 63.1%; Score 164; DB 14; Length 1605;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 164; Conserv 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 97 GCGAGCCCTTACAGCCATGGAGCGCCCTGGAGAGACCCGGTGGCTCCGGAGCTT 156
; Other Information: calponin 1, basic, smooth muscle (CNN1) gene.
; Name/Key: misc_feature
; Location: (1)..(1605)
; Other Information: calponin 1, basic, smooth muscle (CNN1) gene.

US-11-000-688-1504

QY 6 GCGAGCCCTTACAGCCATGGAGCGCCCTGGAGAGACCCGGTGGCTCCGGAGCTT 65

QY 157 CAAAAACATGTGAGGGAGAGGTGTGAGCCGAATTCAGGCCGTGCTCTGTTCTC 216

DB 66 CAAAAACATGTGAGGGAGAGGTGTGAGCCGAATTCAGGCCGTGCTCTGTTCTC 125

QY 97 GCGAGCCCTTACAGCCATGGAGCGCCCTGGAGAGACCCGGTGGCTCCGGAGCTT 156

DB 6 GCGAGCCCTTACAGCCATGGAGCGCCCTGGAGAGACCCGGTGGCTCCGGAGCTT 65

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nucleic - nucleic search, using sw model

on: April 9, 2006, 02:10:27 ; Search time 2800.56 Seconds
(without alignments)
6758.955 Million cell updates/sec

title: US-10-500-173-3
refr. score: 333
sequence: 1 gaaacaatgacacaatcagc.....taagaaacaaggtagggtaggg 333

scoring table: IDENTITY_NUC
Gapop 10⁻⁰ , Gapext 1.0

searched: 5883141 seqs, 2842175653 residues

total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%

ALIGNMENT

Qy	Matches	333; Conservative	0; MiAmAtches	0; Indels	0; Gaps	0;
1	GGAAATGACACATACGCTCCCATACCAAGGGCTGACATCACAGGGAGGGAAAG	60				

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:04:37 ; Search time 482.692 Seconds (without alignments)

4597.840 Million cell updates/sec

Title: US-10-500-173-3

Perfect score: 333

Sequence: 1 gaaacaatgacacaatcaggc.....taagaacaaggtaggggtgg 333

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

1: geneseqn1980b: * .b

2: geneseqn1990b: * .b

3: geneseqn2000b: * .b

4: geneseqn2010b: * .b

5: geneseqn2010bs: * .b

6: geneseqn2002bs: * .b

7: geneseqn2002bs: * .b

8: geneseqn2003as: * .b

9: geneseqn2003bs: * .b

10: geneseqn2003cb: * .b

11: geneseqn2003ds: * .b

12: geneseqn2004ab: * .b

13: geneseqn2004bs: * .b

14: geneseqn2005s: * .b

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB . ID	Description
1	333	100.0	333	10	ADC21272	Pdc21272 Human cal
2	333	100.0	333	10	ADD68311	ADD68311 DNA compr
3	333	100.0	333	10	ADD29395	ADD29395 Human cal
4	333	100.0	333	10	AB270046	AB270046 Human cal
5	276.8	83.1	1206	13	ACN41242	ACN41242 Human dia
6	276.8	83.1	1257	13	ACN41241	ACN41241 Human dia
7	276.8	83.1	1395	13	ACN41239	ACN41239 Human dia
8	276.8	83.1	1395	13	ACN41240	ACN41240 Human dia
9	260	78.1	260	10	ADC21271	ADC21271 Human cel
10	260	78.1	260	10	ADD68310	ADD68310 Human ang
11	260	78.1	260	10	ADD29394	ADD29394 Antiarter
12	260	78.1	260	10	AB270045	AB270045 Oligonucle
13	227.8	68.4	1605	12	ADN04009	ADN04009 Antipori
14	198.8	59.7	1586	12	ADJ56427	ADJ56427 Human cDN
15	163.8	49.2	1522	2	AAQ86719	AAQ86719 Carponin
16	163.8	49.2	1522	2	AAV18663	AAV18663
17	155.8	46.8	1517	6	ABU62318	ABU62318 Colon ade
18	155.8	46.8	1517	6	ABU69488	ABU69488 Prostate
19	155.8	46.8	1517	6	ABT10830	ABT10830 Human bre

ALIGNMENTS

20	141.8	42.6	1499	12	ADQ83552	ADQ83552 Human tum
21	141.8	42.6	1504	4	AAD7354	AAD7354 Human DNA
22	141.8	42.6	1504	8	ABZ4836	ABZ4836 Coding se
23	141.8	42.6	1504	10	ADB75245	ADB75245 Probate
24	141.8	42.6	1504	13	ADP9030	ADP9030 Calponin
25	103.6	31.1	425	9	ACH0634	ACH0634 Human tes
26	89.4	26.8	711	5	ABV14470	ABV14470 Human pro
27	86.5	26.0	156	5	ABV14470	ABV14470 Human pro
28	62.4	18.7	538	6	ABN73703	ABN73703 Bovine em
29	57.8	17.4	698	5	ABV07301	ABV07301 Human pro
30	43.6	13.1	120	10	ABX85881	ABX85881 Corn ear-
31	43.4	13.0	1932	6	ABK33774	ABK33774 Rat sequ
32	43.4	13.0	1932	10	ADP85375	ADP85375 Toxicity-
33	43.4	13.0	1932	10	ADP85375	ADP85375 Primary
34	41.4	13.0	1932	13	ADY41198	ADY41198 Rat cardi
35	43.2	13.0	696	12	AD40452	AD40452 Plant cDN
36	41.6	12.5	6	6	ABL71519	ABL71519 Corn tass
37	41.6	12.5	1499	12	ADNB86965	ADNB86965 Human pro
38	41.2	12.4	283	3	AAC09556	AAC09556 Human sec
39	41.2	12.4	840	14	ADP64918	ADP64918 Novel hum
40	41.2	12.4	1866	12	ABN5249	ABN5249 Novel hum
41	41.2	12.4	2122	6	ABP54264	ABP54264 Gene #174
42	41.2	12.4	2122	13	ADP54264	ADP54264 Human PRO
43	41.2	12.4	2122	14	ADY14592	ADY14592 DNA encod
44	41.2	12.4	2161	8	ACG46585	ACG46585 Human dict
45	41	12.3	41	10	ADC21270	ADC21270 Human cel

RESULT 1

ID ADC21272 Standard; DNA; 333 BP.

XX ADC21272;

AC

DT 18-DEC-2003 (first entry)

XX

DE Human calponin gene promoter with its structural gene fragment.

XX

KW human; cell-specific expression vector; cell-specific replication vector;

KW gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;

KW organ transplantation; arteriosclerosis; diabetic omentopathy; ds;

KW calponin; promoter; structural gene fragment.

XX

OS Homo sapiens.

XX

PN WO2003057888-A1.

XX

PD 17-JUL-2003.

XX

PP 26-DEC-2002; 2002WO-JP011683.

XX

PR 28-DEC-2001; 2001JP-00402102.

PR 30-AUG-2002; 2002JP-00255395.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX

PI Takahashi K, Yamamura H;

XX

DR WPI; 2003-577527/54.

XX

PR Cell-specific expression/replication vector containing transcription

PT initiation regulating domain of human calponin gene, applicable in gene

PT therapy of malignant tumor lung and liver fibrosis or diabetic

PT omentopathy.

XX

PS Claim 4; SEQ ID NO 3; 65PP; Japanese.

XX

CC The invention comprises a cell-specific expression/replication vector

CC which does not act on normal cells. The vector of the invention is useful

CC in gene therapy for the treatment of: malignant tumour, liver fibrosis,

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:12:09 ; Search time 3422.44 Seconds

(without alignment) 4552.334 Million cell updates/sec

Title: US-1.0-500-173-3

Perfect score: 333

Sequence: 1. gaacaatgaccataatcagc.....taagaacaaggtaggggtgg 3.33

Scoring table: IDENTITY_NUC
 GapP 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: 9b_est1:*

2: 9b_est2:*

3: 9b_est3:*

4: 9b_hrc:*

5: 9b_est4:*

6: 9b_est5:*

7: 9b_est6:*

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9: 9b_gbs1:*

10: 9b_gbs2:*

11: 9b_gbs3:*

..b

RESULT 1

BG718473

LOCUS

602696515F1

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GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 13:46:44 ; Search time 163.874 Seconds

(without alignments)
 3612.096 Million cell updates/sec

Title: US-10-500-173-3

Perfect score: 333

Sequence: 1 gaaacatgaccaatcagc.....taagaacaaaggtaggggtgg 333

Scoring table: IDENTITY_NUC

GapP 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	331.4	99.5	15585	3	US-09-949-016-11927		Sequence 11927, A	
2	331.4	99.5	15585	3	US-09-949-016-15627		Sequence 15627, A	
3	141.8	42.6	1504	3	US-09-949-016-185		Sequence 185, AP	
4	141.8	42.6	1504	3	US-09-949-016-185		Sequence 185, AP	
5	45	13.5	33753	3	US-09-949-016-15741		Sequence 15741, A	
6	45	13.5	33756	3	US-09-949-016-12006		Sequence 12006, A	
7	44.4	13.3	15273	3	US-09-949-016-12356		Sequence 12356, A	
8	44.4	13.3	15273	3	US-09-949-016-13341		Sequence 13341, AP	
9	43.6	13.1	120	3	US-09-949-016-4341		Sequence 4341, AP	
10	41.2	12.4	283	3	US-09-513-994A-4341		Sequence 13431, A	
11	41.2	12.4	2122	3	US-09-949-016-614		Sequence 614, AP	
12	41.2	12.4	2122	3	US-09-949-016-159		Sequence 159, AP	
13	40.6	12.2	1589	3	US-09-949-016-399		Sequence 399, AP	
14	40.6	12.2	1607	3	US-09-949-016-264		Sequence 264, AP	
C	36.8	11.1	8186	3	US-10-29-517-19		Sequence 19, App1	
C	36.2	10.9	23187	3	US-09-499-522-1		Sequence 1, App1	
C	34.6	10.4	601	3	US-09-949-016-169734		Sequence 169734, A	
C	34.6	10.4	3510	3	US-09-265-585C-95		Sequence 95, App1	
C	20	34.6	10.4	5962	9	5386025-5		Patent No. 5386025
C	21	34.6	10.4	5975	2	US-08-04-354B-1		Sequence 1, App1
C	22	34.6	10.4	5975	2	US-08-435-75B-1		Sequence 1, App1
C	23	34.6	10.4	5975	2	US-08-336-257A-3		Sequence 3, App1
C	24	34.6	10.4	5975	3	US-08-84-599-1		Sequence 1, App1

ALIGNMENTS

RESULT 1

US-09-949-016-11927

Sequence 11927, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHSMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 11927

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSBQ For Windows Version 4.0

SEQ ID NO 11927

LENGTH: 15585

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc. feature

LOCATION: (11) (11585)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-11927

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Matches 332; Conservative 0;

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Db 1819 GAACAAATGACAAATCAGCTCCAAATACCAAGGGCTGACATCAGCCATGGAAAGGG 1878

Query Match 99.5%; Score 331.4; DB 3; Length 15585;

Best Local Similarity 99.7%; Prod. No. 5.0e-83; Mismatches 0; Gaps 0;

Matches 332; Conservative 0;

Query 1

GAACAAATGACAAATCAGCTCCAAATACCAAGGGCTGACATCAGCCATGGAAAGGG 120

Db 1879 GAACAAATGACAAATCAGCTCCAAATACCAAGGGCTGACATCAGCCATGGAAAGGG 1938

Query 121 CGGCCCTGAAAGAACCCGGTGGCTCTGACCTCAACATGCTGAGGGAGGG 180

Db 1939 CGGCCCTGAAAGAACCCGGTGGCTCTGACCTCAACATGCTGAGGGAGGG 1938

Query 181 TGGCAGGGAACTCAGCCGCTGCTGCTGAGGGAGGG 240

ALIGNMENTS

Maximum Match 100% Listing first 45 summaries						
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3: /cgn2_6_ptodata/1/pubpna/us09a_pubcomb.seq*						
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES					
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2	333	100.0	333	8	US-10-500-173-3	
3	260	78.1	260	8	US-10-477-797-2	
4	260	78.1	260	8	US-10-500-173-2	
5	206.8	62.1	1580	6	US-10-062-674-1778	
6	198.8	59.7	1586	5	US-10-084-817-233	
7	155.8	46.8	1517	3	US-03-969-708-354	
8	155.8	46.8	1517	3	US-09-873-367C-655	
9	155.8	46.8	1517	7	US-10-240-425-1209	
10	155.8	46.8	1517	9	US-10-843-641A-655	
11	155.8	46.8	1517	9	US-10-843-641A-7825	
12	155.8	46.8	1517	9	US-10-756-149-3969	
13	141.8	42.6	1504	8	US-10-205-823-59	
14	141.8	42.6	1504	8	US-10-788-792-36	
15	141.8	42.6	1504	8	US-10-473-974-194	
16	141.8	42.6	1504	10	US-11-0945-454-69	
17	103.6	31.1	425	3	US-09-918-995-17846	
18	89.4	26.8	711	8	US-10-357-930-14461	
19	86.6	24.6	156	8	US-10-357-930-15569	
20	62.4	18.7	538	3	US-09-876-143-638	
21	57.8	17.4	648	8	US-10-357-930-5292	
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; GENERAL INFORMATION						
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION						
; TITLE OF INVENTION: Application Vector Showing Cell-Specific Expression						
; FILE REFERENCE: K01002PCT						
; CURRENT APPLICATION NUMBER: US/10/477,797						
; CURRENT FILING DATE: 2003-11-13						
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; PRIORITY FILING DATE: 2001-05-14						
; SOFTWARE: PatentIn Ver. 2.1						
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; LENGTH: 333						
; TYPE: DNA						
; ORGANISM: Artificial Sequence						
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GenCore version 5.1.7									
Copyright (c) 1993 - 2006 Biocceleration Ltd.									
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1 227.8 68.4 1605 14 US-11-000-588-1504 Sequence 1504, Ap									
2 141.8 42.6 1504 11 US-11-245-147-194 Sequence 194, Ap									
3 66.2 19.9 1498 14 US-11-136-527-3031 Sequence 303, Ap									
4 44.6 13.2 2271 14 US-11-136-527-2536 Sequence 2536, Ap									
5 44.4 13.3 168516 14 US-11-121-086-3 Sequence 3, Appl									
6 40.6 12.2 736 8 US-10-75-185-61962 Sequence 61962, A									
7 40.6 12.2 736 10 US-10-750-631-61962 Sequence 61962, A									
8 40.6 12.2 1607 14 US-11-000-888-1008 Sequence 1008, Ap									
9 40.2 12.1 1400 14 US-11-13-527-7127 Sequence 7127, Ap									
10 36.8 11.1 1084 9 US-10-517-636-82 Sequence 82, Appl									
11 36.8 11.1 1582 11 US-11-050-557-454 Sequence 454, Appl									
12 36.8 11.1 1582 11 US-11-043-006-59 Sequence 59, Appl									
13 36.2 10.9 2187 11 US-11-236-136-98-1 Sequence 1, Appl									
14 35.8 10.8 627 10 US-10-301-880-39363 Sequence 239163, Ap									
15 35.8 10.8 627 10 US-10-140-880-82772 Sequence 852772, Ap									
16 35.8 10.8 635 6 US-09-225-054-142693 Sequence 144833, Ap									
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